

0270

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/677,752

DATE: 10/12/2000
 TIME: 18:31:08

ENTERED

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\10122000\I677752.raw

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4 <110> APPLICANT: W. James Jackson
6 <120> TITLE OF INVENTION: Chlamydia sp PROTEIN, GENE SEQUENCE AND
7   USES THEREOF
9 <130> FILE REFERENCE: 7969-087
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/677,752
C--> 11 <141> CURRENT FILING DATE: 2000-10-03
11 <160> NUMBER OF SEQ ID NOS: 71
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 2898
17 <212> TYPE: DNA
18 <213> ORGANISM: Chlamydia sp
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)...(2895)
24 <400> SEQUENCE: 1
25 atg aaa aaa gcg ttt ttc ttt ttc ctt att gga aac tcc cta tca gga      48
26 Met Lys Lys Ala Phe Phe Phe Phe Leu Ile Gly Asn Ser Leu Ser Gly
27   1           5           10          15
29 cta gct aga gag gtt cct tct aga atc ttt ctt atg ccc aac tca gtt      96
30 Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val
31   20          25          30
33 cca gat cct acg aaa gag tcg cta tca aat aaa att agt ttg aca gga      144
34 Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly
35   35          40          45
37 gac act cac aat ctc act aac tgc tat ctc gat aac cta cgc tac ata      192
38 Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile
39   50          55          60
41 ctg gct att cta caa aaa act ccc aat gaa gga gct gct gtc aca ata      240
42 Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile
43   65          70          75          80
45 aca gat tac cta agc ttt ttt gat aca caa aaa gaa ggt att tat ttt      288
46 Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe
47   85          90          95
49 gca aaa aat ctc acc cct gaa agt ggt ggt gcg att ggt tat gcg agt      336
50 Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser
51   100         105         110
53 ccc aat tct cct acc gtg gag att cgt gat aca ata ggt cct gta atc      384
54 Pro Asn Ser Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile
55   115         120         125
57 ttt gaa aat aat act tgt tgc aga cca ttt aca tcg agt aat cct aat      432
58 Phe Glu Asn Asn Thr Cys Cys Arg Pro Phe Thr Ser Ser Asn Pro Asn
59   130         135         140
61 gca gct gtt aat aaa ata aga gaa ggc gga gcc att cat gct caa aat      480
62 Ala Ala Val Asn Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn
63   145         150         155         160
65 ctt tac ata aat cat aat cat gat gtg gtc gga ttt atg aag aac ttt      528

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66	Leu	Tyr	Ile	Asn	His	Asn	His	Asp	Val	Val	Gly	Phe	Met	Lys	Asn	Phe	
67				165					170						175		
69	tct	tat	gtc	cga	gga	gga	gcc	att	agt	acc	gct	aat	acc	ttt	gtt	gtg	576
70	Ser	Tyr	Val	Arg	Gly	Gly	Ala	Ile	Ser	Thr	Ala	Asn	Thr	Phe	Val	Val	
71				180					185					190			
73	agc	gag	aat	cag	tct	tgt	ttt	ctc	ttt	atg	gac	aac	atc	tgt	att	caa	624
74	Ser	Glu	Asn	Gln	Ser	Cys	Phe	Leu	Phe	Met	Asp	Asn	Ile	Cys	Ile	Gln	
75				195				200						205			
77	act	aat	aca	gca	gga	aaa	ggg	ggc	gct	atc	tat	gct	gga	acg	agc	aat	672
78	Thr	Asn	Thr	Ala	Gly	Lys	Gly	Gly	Ala	Ile	Tyr	Ala	Gly	Thr	Ser	Asn	
79				210				215						220			
81	tct	ttt	gag	agt	aat	aac	tgc	gat	ctc	ttc	ttt	atc	aat	aac	gcc	tgt	720
82	Ser	Phe	Glu	Ser	Asn	Asn	Cys	Asp	Leu	Phe	Phe	Ile	Asn	Asn	Ala	Cys	
83				225			230							235		240	
85	tgt	gca	gga	gga	gcg	atc	ttc	tcc	cct	atc	tgt	tct	cta	aca	gga	aat	768
86	Cys	Ala	Gly	Gly	Ala	Ile	Phe	Ser	Pro	Ile	Cys	Ser	Leu	Thr	Gly	Asn	
87					245					250				255			
89	cgt	ggg	aac	atc	gtt	ttc	tat	aac	aat	cgc	tgc	ttt	aaa	aat	gta	gaa	816
90	Arg	Gly	Asn	Ile	Val	Phe	Tyr	Asn	Asn	Arg	Cys	Phe	Lys	Asn	Val	Glu	
91				260					265					270			
93	aca	gct	tct	tca	gaa	gct	tct	gat	gga	gga	gca	att	aaa	gta	act	act	864
94	Thr	Ala	Ser	Ser	Glu	Ala	Ser	Asp	Gly	Gly	Ala	Ile	Lys	Val	Thr	Thr	
95				275				280						285			
97	cgc	cta	gat	gtt	aca	ggc	aat	cgt	ggg	agg	atc	ttt	ttt	agt	gac	aat	912
98	Arg	Leu	Asp	Val	Thr	Gly	Asn	Arg	Gly	Arg	Ile	Phe	Phe	Ser	Asp	Asn	
99				290				295					300				
101	atc	aca	aaa	aat	tat	ggc	gga	gct	att	tac	gct	cct	gta	gtt	acc	cta	960
102	Ile	Thr	Lys	Asn	Tyr	Gly	Gly	Ala	Ile	Tyr	Ala	Pro	Val	Val	Thr	Leu	
103				305			310					315				320	
105	gtg	gat	aat	ggc	cct	acc	tac	ttt	ata	aac	aat	atc	gcc	aat	aat	aag	1008
106	Val	Asp	Asn	Gly	Pro	Thr	Tyr	Phe	Ile	Asn	Asn	Ile	Ala	Asn	Asn	Lys	
107					325					330					335		
109	ggg	ggc	gct	atc	tat	ata	gac	gga	acc	agc	aac	tcc	aaa	att	tct	gcc	1056
110	Gly	Gly	Ala	Ile	Tyr	Ile	Asp	Gly	Thr	Ser	Asn	Ser	Lys	Ile	Ser	Ala	
111				340					345					350			
113	gac	cgc	cat	gct	att	att	ttt	aat	gaa	aat	att	gtg	act	aat	gta	act	1104
114	Asp	Arg	His	Ala	Ile	Ile	Phe	Asn	Glu	Asn	Ile	Val	Thr	Asn	Val	Thr	
115				355				360						365			
117	aat	gca	aat	ggg	acc	agt	acg	tca	gct	aat	cct	cct	aga	aga	aat	gca	1152
118	Asn	Ala	Asn	Gly	Thr	Ser	Thr	Ser	Ala	Asn	Pro	Pro	Arg	Arg	Asn	Ala	
119				370				375					380				
121	ata	aca	gta	gca	agc	tcc	tct	ggg	gaa	att	cta	tta	gga	gca	ggg	agt	1200
122	Ile	Thr	Val	Ala	Ser	Ser	Ser	Gly	Glu	Ile	Leu	Leu	Gly	Ala	Gly	Ser	
123				385				390					395			400	
125	agc	caa	aat	tta	att	ttt	tat	gat	cct	att	gaa	gtt	agc	aat	gca	ggg	1248
126	Ser	Gln	Asn	Leu	Ile	Phe	Tyr	Asp	Pro	Ile	Glu	Val	Ser	Asn	Ala	Gly	
127					405					410					415		
129	gtc	tct	gtg	tcc	ttc	aat	aag	gaa	gct	gat	caa	aca	ggc	tct	gta	gta	1296
130	Val	Ser	Val	Ser	Phe	Asn	Lys	Glu	Ala	Asp	Gln	Thr	Gly	Ser	Val	Val	

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131		420		425		430			
133	ttt	tca	gga	gct	act	gtt	aat	tct	gca
134	Phe	Ser	Gly	Ala	Thr	Val	Asn	Ser	Ala
135			435				440		
137	caa	aca	aaa	aca	cct	gca	ccc	ctt	act
138	Gln	Thr	Lys	Thr	Pro	Ala	Pro	Leu	Thr
139		450					455		
141	atc	gaa	gat	cat	gct	cag	ctt	aca	gtg
142	Ile	Glu	Asp	His	Ala	Gln	Leu	Thr	Val
143		465					470		
145	ggg	gtt	gtt	tct	ctt	ggg	aat	gga	gca
146	Gly	Val	Val	Ser	Leu	Gly	Asn	Gly	Ala
147				485				490	
149	ggg	gca	gga	aat	tct	gct	agc	aat	gcc
150	Gly	Ala	Gly	Asn	Ser	Ala	Ser	Asn	Ala
151			500				505		
153	gga	ttg	aat	ctt	tct	tcc	att	ctg	aaa
154	Gly	Leu	Asn	Leu	Ser	Ser	Ile	Leu	Lys
155			515				520		
157	ttg	tgg	gta	gag	cct	aca	aat	aac	agc
158	Leu	Trp	Val	Glu	Pro	Thr	Asn	Asn	Ser
159		530					535		
161	gca	gct	acc	ttt	tca	tta	agt	gat	gta
162	Ala	Ala	Thr	Phe	Ser	Leu	Ser	Asp	Val
163		545					550		
165	tat	ggg	aat	tct	cct	tat	gaa	tcc	aca
166	Tyr	Gly	Asn	Ser	Pro	Tyr	Glu	Ser	Thr
167				565				570	
169	tca	cag	cct	atg	cta	tct	att	tct	gag
170	Ser	Gln	Pro	Met	Leu	Ser	Ile	Ser	Glu
171			580					585	
173	tct	gat	gat	atg	gat	ttt	tgg	gga	cta
174	Ser	Asp	Asp	Met	Asp	Phe	Ser	Gly	Leu
175			595					600	
177	caa	gga	ctt	tgg	act	tgg	ggc	tgg	gca
178	Gln	Gly	Leu	Trp	Thr	Trp	Gly	Trp	Ala
179		610					615		
181	gca	tct	tca	gca	aca	atc	aca	gat	cca
182	Ala	Ser	Ser	Ala	Thr	Ile	Thr	Asp	Pro
183		625						630	
185	aga	acc	tta	tta	ctg	act	tgg	ctt	cct
186	Arg	Thr	Leu	Leu	Leu	Thr	Trp	Leu	Pro
187			645					650	
189	aaa	cac	aga	agt	ccc	ctc	ata	gcg	aat
190	Lys	His	Arg	Ser	Pro	Leu	Ile	Ala	Asn
191			660					665	
193	ctt	gca	aca	gaa	agc	tta	aaa	aat	agt
194	Leu	Ala	Thr	Glu	Ser	Leu	Lys	Asn	Ser
195			675					680	
									685

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197	cat cct ttc tgg gga att aca gga gga gga cta ggc atg atg gtt tac	2112
198	His Pro Phe Trp Gly Ile Thr Gly Gly Gly Leu Gly Met Met Val Tyr	
199	690 695 700	
201	caa gat cct cga gaa aat cat cct gga ttc cat atg cgc tct tcc gga	2160
202	Gln Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly	
203	705 710 715 720	
205	tac tct gcg ggg atg ata gca ggg cag aca cac acc ttc tca ttg aaa	2208
206	Tyr Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys	
207	725 730 735	
209	ttc agt cag acc tac acc aaa ctc aat gag cgt tac gca aaa aac aac	2256
210	Phe Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn	
211	740 745 750	
213	gta tct tct aaa aat tac tca tgc caa gga gaa atg ctc ttc tca ttg	2304
214	Val Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu	
215	755 760 765	
217	caa gaa ggt ttc ttg ctg act aaa tta gtt ggg ctt tac agc tat gga	2352
218	Gln Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly	
219	770 775 780	
221	gac cat aac tgt cac cat ttc tat acc caa gga gaa aat cta aca tct	2400
222	Asp His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser	
223	785 790 795 800	
225	caa ggg acg ttc cgt agt caa acg atg gga ggt gct gtt ttt ttt gat	2448
226	Gln Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp	
227	805 810 815	
229	ctc cct atg aaa ccc ttt gga tca acg cat ata ctg aca gct ccc ttt	2496
230	Leu Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe	
231	820 825 830	
233	tta ggt gct ctt ggt att tat tct agc ctg tct cac ttt act gag gtg	2544
234	Leu Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val	
235	835 840 845	
237	gga gcc tat ccg cga agc ttt tct aca aag act cct ttg atc aat gtc	2592
238	Gly Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val	
239	850 855 860	
241	cta gtc cct att gga gtt aaa ggt agc ttt atg aat gct acc caa aga	2640
242	Leu Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr Gln Arg	
243	865 870 875 880	
245	cct caa gcc tgg act gta gaa ttg gca tac caa ccc gtt ctg tat aga	2688
246	Pro Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg	
247	885 890 895	
249	caa gaa cca ggg atc gcg acc cag ctc cta gcc agt aag ggt att tgg	2736
250	Gln Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp	
251	900 905 910	
253	ttt ggt agt gga agc ccc tca tgc cgt cat gcc atg tcc tat aaa atc	2784
254	Phe Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile	
255	915 920 925	
257	tca cag caa aca caa cct ttg agt tgg tta act ctc cat ttc cag tat	2832
258	Ser Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr	
259	930 935 940	
261	cat gga ttc tac tcc tct tca acc ttc tgt aat tat ctc aat ggg gaa	2880

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date



Creation date: 11-24-2003
Indexing Officer: PDO1 - PHU DO
Team: OIPEBackFileIndexing
Dossier: 09677752

Legal Date: 02-07-2001

No.	Doccode	Number of pages
1	IDS	2
2	FOR	293

Total number of pages: 295

Remarks:

Order of re-scan issued on